Differences in the intestinal microbiome of healthy children and patients with newly diagnosed Crohn's disease

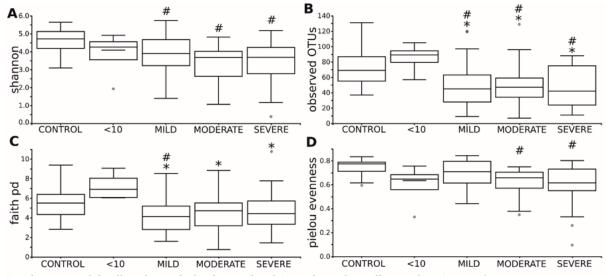
Kinga Kowalska-Duplaga¹, Tomasz Gosiewski², Przemysław Kapusta³, Agnieszka Sroka-Oleksiak^{2,4}, Andrzej Wędrychowicz¹, Stanisław Pieczarkowski¹, Agnieszka H. Ludwig-Słomczyńska³, Paweł P. Wołkow³, Krzysztof Fyderek¹.

¹Department of Pediatrics, Gastroenterology and Nutrition, Faculty of Medicine, Jagiellonian University Medical College, Kraków, Poland

²Division of Molecular Medical Microbiology, Department of Microbiology, Faculty of Medicine, Jagiellonian University Medical College, Kraków, Poland

³Center for Medical Genomics – OMICRON, Jagiellonian University Medical College, Kraków, Poland

⁴Division of Mycology, Department of Microbiology, Faculty of Medicine, Jagiellonian University Medical College, Kraków, Poland



Supplement 1. Alpha diversity analysis of control and CD patients depending on the PCDAI scale.

Figure legend:

Supplementary Figure S1. Alpha diversity analysis of control and CD patients depending on the PCDAI scale. Within-sample diversity measured by Shannon index (A), observed OTUs (B), Faith's phylogenetic diversity (C) and Pielou's measure of species evenness (D). Kruskal-Wallis with Post-hoc was performed to analyse statistical significance. Statistically significant values between control and other groups were represented as "#". Statistically significant values between PCDAI <10 group and with other groups: mild (10–27.5 points; 21 patients), moderate (>27.5–39 points, 17 patients) and severe (>40 points; 21 patients) CD disease activity (Supplementary Figure S1 online) were represented as "*".